1. (currently amended) A method for cloning at least one of a restriction endonuclease or a methyl transferase gene, ~~one or more prokaryotic genes in~~ from a cassette array, ~~the array being characterized by a plurality of genes where each gene is embedded in a predictable nucleotide sequence context including a repeat DNA sequence,~~ the method comprising the steps of:

(a) hybridizing oligonucleotide primers having sequences contained in at least one of SEQ ID. No. 5 through SEQ ID. No 91, to ~~identified~~ flanking repeat sequences in the cassette array, wherein the cassette array is a plurality of genes such that each gene is embedded in a predictable nucleotide sequence context including a repeat DNA sequence;

(b) amplifying the DNA between the hybridized primers of step (a) to produce DNA fragments which contain one or more genes; ~~and~~

(c) ligating the DNA fragments of step (b) into a vector for cloning, the one or more genes in a host cell; and~~.~~

(d) determining whether the cloned DNA fragments encode at least one of a restriction endonuclease or a methyl transferase.

2-4. (canceled)

5. (original) The method of claim 1 wherein said oligonucleotides contain recognition sites which permit directional cloning.

6. (original) The method of claim 5 wherein the DNA fragments are ligated into said vector in an orientation that enables expression.

7. (currently amended) A method for identifying the presence of a gene cassette array~~s~~ from within a prokaryotic target DNA preparation, said method comprising the steps of:

(a) hybridizing at least one oligonucleotide to a prokaryotic DNA preparation, ~~which hybridizes to one or more of SEQ ID NO:5 through SEQ ID NO:78 to a DNA preparation~~ wherein the at least one oligonucleotide is capable of hybridizing under stringent conditions to one or more DNA sequences selected from SEQ ID NO:5 through SEQ ID NO:91; ~~and~~

(b) detecting the presence of a stable DNA-DNA hybrid~~.~~ , so as to identify at least one gene cassette array, wherein the cassette array is a plurality of genes such that each gene is embedded in a predictable nucleotide sequence context including a repeat DNA sequence; and

(c) identifying the presence of the gene cassette array from within the prokaryotic target DNA preparation.

8. (original) The method of claim 7 wherein said detection comprises determining the presence of stable DNA-DNA hybrid by Southern blot or dot blot.

9. (original) The method of claim 7 wherein said detection comprises employing at least two oligonucleotides and hybridizing said oligonucleotides to said DNA preparation, and detecting their ability to support DNA polymerization at the 3′ end of the stable DNA-DNA hybrid.

10. (original) The method of claim 7 wherein said oligonucleotides comprise SEQ ID NO:79 through SEQ ID NO:91.

11. (canceled)

12. (original) The method of claim 7 wherein the DNA source comprises an individual strain.

13. (original) The method of claim 7 wherein the DNA source comprises a group or pool of strains.

14. (original) The method of claim 7 wherein the DNA source comprises environmental DNA.

Claims 15-16 (cancelled).

17. (withdrawn) A method for identifying gene cassette arrays from a predetermined DNA sequence, said method comprising the steps of:

(a) screening the said predetermined DNA sequence for TAACWA;

(b) screening the said predetermined DNA sequence for CGTTRR;

(c) screening for DNA segments wherein the 5′ T of step A is less than about 200 base pairs form the 3′ R of step B; and

(d) determining whether the DNA sequence of step C is repeated in the predetermined DNA sequence.

18. (previously presented) The method of claim 2, wherein the adhesins are fimbrial proteins.

19. (previously presented) The method according to claim 2, wherein the signaling peptides are kinases.

20. (previously presented) The method according to claim 2, wherein the detoxifying enzymes are drug resistance determinants.